

Amendments to the Claims:

1. (Canceled)

2. (Currently amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1 or 3;
- (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 4;
- (c) a nucleotide sequence encoding residues ~~1-266~~ 1-265 of the amino acid sequence set forth in SEQ ID NO: 2 or 4;
- (d) an antisense nucleotide sequence corresponding to the nucleotide sequence of (a), (b) or (c);
- (e) a nucleotide sequence comprising at least 85% sequence identity to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3[[]], wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3;
- (f) a nucleotide sequence comprising at least 50 contiguous nucleotides of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3[[]], wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity;
- (g) a nucleotide sequence that hybridizes under stringent conditions to the complement of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3[[]], wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and said stringent conditions comprise hybridization in a solution comprising 50%

formamide, 1 M NaCl, and 1% SDS at 37°C and a wash in a solution comprising 0.1X SSC at 60°C; and

- (h) a nucleotide sequence encoding a fragment or variant of the amino acid sequence set for in SEQ ID NO: 2 or 4, wherein said fragment or said variant confers a dominant-negative phenotype in a host cell[[.]] and has at least 85% sequence identity to at least one amino acid sequence selected from the group consisting of the amino acid sequences set forth in SEQ ID NOS: 2 and 4, and wherein percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3;
- (i) a nucleotide sequence encoding an amino acid sequence having at least 85% sequence identity to at least one amino acid sequence selected from the group consisting of the amino acid sequences set forth in SEQ ID NOS: 2 and 4, wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3; and
- (j) nucleotides 1-797 of SEQ ID NO: 1.

3. (Canceled)

4. (Currently amended) An expression cassette comprising a promoter operably linked to the ~~nucleotide sequence~~ nucleic acid molecule of claim 2.

5. (Original) The expression cassette of claim 4, wherein said promoter drives expression in a plant.

6. (Original) The expression cassette of claim 5, wherein said promoter is selected from the group consisting of constitutive, pathogen-inducible, insect-inducible, wound-inducible, tissue-preferred, and developmentally regulated promoters.

7. (Canceled)

8. (Canceled)

9. (Currently amended) A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter that drives expression in a plant operably linked to the ~~nucleotide~~ nucleic acid molecule of claim 2.

10. (Original) The plant of claim 9, wherein said promoter is selected from the group consisting of constitutive, tissue-preferred and developmentally regulated promoters.

11. (Original) The plant of claim 9, wherein said plant is a monocot.

12. (Original) The plant of claim 11, wherein said monocot is selected from the group consisting of maize, wheat, rice, sorghum, barley, millet and rye.

13. (Original) The plant of claim 9, wherein said plant is a dicot.

14. (Original) The plant of claim 13, wherein said dicot is selected from the group consisting of tobacco, tomato, potato, soybean, *Brassica* sp., alfalfa, safflower, sunflower, cotton, and peanut.

15. (Original) Transformed seed of the plant of claim 9.

16. (Currently amended) A transformed plant cell comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter that drives expression in a plant cell operably linked to the ~~nucleotide~~ nucleic acid molecule of claim 2.

17. (Canceled)

18. (Canceled)

19. (Currently amended) A method for altering recombination frequency in a plant comprising introducing into a plant the ~~nucleotide~~ nucleic acid molecule of claim 2, wherein the said recombination frequency is increased or decreased in said plant or at least one cell thereof.

20. (Currently amended) The method of claim 19, wherein said ~~nucleotide construct~~ further comprises nucleic acid molecule is operably linked to a promoter that drives expression in a plant cell, ~~said promoter operably linked to said nucleotide sequence.~~

21. (Currently amended) The method of claim 20, wherein said promoter is operably linked to said ~~nucleotide sequence~~ nucleic acid molecule for the production of antisense transcripts.

22. (Original) The method of claim 20, wherein said promoter is selected from the group consisting of constitutive, tissue-preferred and developmentally regulated promoters.

23. (Original) The method of claim 19, wherein said plant or at least one cell thereof comprises a dominant negative phenotype.

24. (Canceled)

25. (Currently amended) The method of claim 19, ~~wherein further comprising~~ efficiency of chimeraplasty[[.]] is increased in said plant or at least one cell thereof.

26. (Currently amended) A method for altering DNA repair processes in a plant comprising introducing into a plant a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1 or 3;
- (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 4;
- (c) a nucleotide sequence encoding residues ~~1-266~~ 1-265 of the amino acid sequence set forth in SEQ ID NO: 2 or 4;
- (d) an antisense nucleotide sequence corresponding to the nucleotide sequence of (a), (b) or (c);
- (e) a nucleotide sequence comprising at least 85% sequence identity to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3[[:]], wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3;
- (f) a nucleotide sequence comprising at least 50 contiguous nucleotides of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3[[:]], wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity;
- (g) a nucleotide sequence that hybridizes under stringent conditions to the complement of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3[[:]], wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and said stringent conditions comprise hybridization in a solution comprising 50% formamide, 1 M NaCl, and 1% SDS at 37°C and a wash in a solution comprising 0.1X SSC at 60°C; and
- (h) a nucleotide sequence encoding a fragment or variant of the amino acid sequence set for in SEQ ID NO: 2 or 4, wherein said fragment or said

variant confers a dominant-negative phenotype in a host cell[[:]]and has at least 85% sequence identity to at least one amino acid sequence selected from the group consisting of the amino acid sequences set forth in SEQ ID NOS: 2 and 4, and wherein percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3;

- (i) a nucleotide sequence encoding an amino acid sequence having at least 85% sequence identity to at least one amino acid sequence selected from the group consisting of the amino acid sequences set forth in SEQ ID NOS: 2 and 4, wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3; and

- (j) nucleotides 1-797 of SEQ ID NO: 1;

wherein the mutation rate of at least one gene in said plant is increased or decreased.

27. (Original) The method of claim 26, wherein the efficiency of gene modification in said plant is increased.

28. (Currently amended) The method of claim 27, wherein ~~said gene modification~~ comprises efficiency of chimeraplasty[[:]] is increased in said plant.

29. (Currently amended) The method of claim 26, wherein ~~said DNA repair process~~ comprises mismatch repair[[:]] is altered in said plant.

30. (Original) The method of claim 26 further comprising operably linking to said nucleotide sequence a promoter that drives expression in a plant cell.

31. (Original) The method of claim 30, wherein said promoter is selected from the group consisting of constitutive, tissue-preferred and developmentally regulated promoters.

32. (Original) The method of claim 26 further comprising introducing a dominant negative mutation into said nucleotide sequence.

33. (Currently amended) The method of claim 26, wherein said nucleic acid molecule confers plant or at least one cell thereof comprises a dominant negative phenotype[[]] on said plant or at least one cell thereof.

34. (Canceled)

35. (Currently amended) The method of claim 26, wherein further comprising efficiency of chimera-plasty[[]] is increased in said plant.

36. (Currently amended) A non-human host cell comprising in its genome a nucleotide construct comprising the ~~nucleotide~~ nucleic acid molecule of claim 2.

37. (Currently amended) The host cell of claim 36, wherein said nucleotide construct further comprises an operably linked promoter that is capable of driving expression of said ~~nucleotide sequence~~ nucleic acid molecule in said host cell.

38. (New) An isolated nucleic acid molecule comprising a nucleotide sequence having at least 90% sequence identity to at least one nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in SEQ ID NOS: 1 and 3, wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3.

39. (New) The nucleic acid molecule of claim 38, wherein said sequence identity is at least 95%.

40. (New) A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter that drives expression in a plant operably linked to the nucleic acid molecule of claim 38.

41. (New) An isolated nucleic acid molecule comprising a nucleotide sequence encoding an amino acid sequence having at least 90% sequence identity to at least one amino acid sequence selected from the group consisting of the amino acid sequences set forth in SEQ ID NOS: 2 and 4, wherein said nucleotide sequence encodes a protein comprising mismatch-repair activity and percent sequence identity is obtained using GAP version 10 with a GAP Weight of 50 and a Length Weight of 3.

42. (New) The nucleic acid molecule of claim 41, wherein said sequence identity is at least 95%.

43. (New) A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter that drives expression in a plant operably linked to the nucleic acid molecule of claim 41.